Search Page 13

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 NEWS  2  Apr 08   "Ask CAS" for self-help around the clock
 NEWS  3  Apr 09   BEILSTEIN: Reload and Implementation of a New Subject Area
 NEWS  4  Apr 09   ZDB will be removed from STN
 NEWS  5  Apr 19   US Patent Applications available in IFICDB, IFIPAT, and IFIUDB
 NEWS  6  Apr 22   Records from IP.com available in CAPLUS, HCAPLUS, and ZCAPLUS
 NEWS  7  Apr 22   BIOSIS Gene Names now available in TOXCENTER
 NEWS  8  Apr 22   Federal Research in Progress (FEDRIP) now available
 NEWS  9  Jun 03   New e-mail delivery for search results now available
 NEWS 10  Jun 10   MEDLINE Reload
 NEWS 11  Jun 10   PCTFULL has been reloaded
 NEWS 12  Jul 02   FOREGE no longer contains STANDARDS file segment
 NEWS 13  Jul 22   USAN to be reloaded July 28, 2002;
                   saved answer sets no longer valid
 NEWS 14  Jul 29   Enhanced polymer searching in REGISTRY
 NEWS 15  Jul 30   NETFIRST to be removed from STN
 NEWS 16  Aug 08   CANCERLIT reload
 NEWS 17  Aug 08   PHARMAMarketLetter(PHARMAML) - new on STN
 NEWS 18  Aug 08   NTIS has been reloaded and enhanced

 NEWS EXPRESS  February 1 CURRENT WINDOWS VERSION IS V6.0d,
               CURRENT MACINTOSH VERSION IS V6.0a(ENG) AND V6.0Ja(JP),
               AND CURRENT DISCOVER FILE IS DATED 05 FEBRUARY 2002
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                                                       ENTRY    SESSION
FULL ESTIMATED COST                                     0.21       0.21

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=> s folding problem
L1          322 FOLDING PROBLEM

=> s l1 and review/dt
L2           36 L1 AND REVIEW/DT

=> duplicate remove l2
PROCESSING COMPLETED FOR L2
L3           36 DUPLICATE REMOVE L2 (0 DUPLICATES REMOVED)

=> d 1-10 bib ab

L3   ANSWER 1 OF 36     MEDLINE
AN   2002109222     MEDLINE
DN   21829853   PubMed ID: 11840678
TI   NMR structural study of disulfide intermediates of hen lysozyme: toward
     unraveling the protein folding problem.
AU   Segawa Shin-ichi; Noda Yasuo; Yokota Atsushi; Tachibana
     Hidekishsegawa@kwansei.ac.jp
SO   TANPAKUSHITSU KAKUSAN KOSO. PROTEIN, NUCLEIC ACID, ENZYME, (2002 Feb) 47
     (2) 145-51.  Ref: 8
     Journal code: 0413762. ISSN: 0039-9450.
CY   Japan
DT   Journal; Article; (JOURNAL ARTICLE)
       General Review; (REVIEW)
     (REVIEW, TUTORIAL)
LA   Japanese
FS   Priority Journals
EM   200203
ED   Entered STN: 20020214
     Last Updated on STN: 20020401
     Entered Medline: 20020326

L3   ANSWER 2 OF 36     MEDLINE
AN   2001678596     MEDLINE
DN   21574594   PubMed ID: 11717420
TI   Structural genomics: an approach to the protein folding
     problem.
AU   Montelione G T
CS   Center for Advanced Biotechnology and Medicine, Department of Molecular
     Biology and Biochemistry, Rutgers University, Piscataway, NJ 08854-5638,
     USA.. guy@cabm.rutgers.edu
NC   P50-GM62413 (NIGMS)
SO   PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF
     AMERICA, (2001 Nov 20) 98 (24) 13488-9.  Ref: 17
     Journal code: 7505876. ISSN: 0027-8424.
CY   United States
DT   Journal; Article; (JOURNAL ARTICLE)
       General Review; (REVIEW)
     (REVIEW, TUTORIAL)
LA   English
FS   Priority Journals
EM   200201
ED   Entered STN: 20011129
     Last Updated on STN: 20020125
     Entered Medline: 20020108
```

L3 ANSWER 3 OF 36 MEDLINE
AN 2002071546 MEDLINE
DN 21656358 PubMed ID: 11798093
TI In vitro studies of membrane protein folding.
AU Booth P J; Templer R H; Meijberg W; Allen S J; Curran A R; Lorch M
CS Department of Biochemistry, School of Medical Sciences, University Walk, Bristol, UK.. paula.booth@bristol.ac.uk
SO CRITICAL REVIEWS IN BIOCHEMISTRY AND MOLECULAR BIOLOGY, (2001) 36 (6) 501-603. Ref: 299
Journal code: 8903774. ISSN: 1040-9238.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, ACADEMIC)
LA English
FS Priority Journals
EM 200206
ED Entered STN: 20020125
Last Updated on STN: 20020606
Entered Medline: 20020605
AB The study of membrane protein folding is a new and challenging research field. Consequently, there are few direct studies on the in vitro folding of membrane proteins. This review covers work aimed at understanding folding mechanisms and the intermolecular forces that drive the folding of integral membrane proteins. We discuss the kinetic and thermodynamic studies that have been undertaken. Our review also draws on closely related research, mainly from purification studies of functional membrane proteins, and gives an overview of some of the successful methods. A brief survey is also given of the large body of mutagenesis and fragment work on membrane proteins, as this too has relevance to the **folding problem**. It is noticeable that the choice of solubilizing detergents and lipids can determine the success of the method, and indeed it appears that particular lipid properties can be used to control the rate and efficiency of folding. This has important ramifications for much in vitro folding work in that it aids our understanding of how to obtain and handle folded, functional protein. With this in mind, we also cover some relevant properties of model, lipid-bilayer systems.

L3 ANSWER 4 OF 36 MEDLINE
AN 2001402919 MEDLINE
DN 21347076 PubMed ID: 11455545
TI Generalized-ensemble algorithms for molecular simulations of biopolymers.
AU Mitsutake A; Sugita Y; Okamoto Y
CS Department of Theoretical Studies, Institute for Molecular Science, Okazaki, Aichi, Japan.
SO BIOPOLYMERS, (2001) 60 (2) 96-123. Ref: 140
Journal code: 0372525. ISSN: 0006-3525.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, ACADEMIC)
LA English
FS Priority Journals
EM 200109
ED Entered STN: 20010924
Last Updated on STN: 20010924
Entered Medline: 20010920
AB In complex systems with many degrees of freedom such as peptides and proteins, there exists a huge number of local-minimum-energy states. Conventional simulations in the canonical ensemble are of little use, because they tend to get trapped in states of these energy local minima. A simulation in generalized ensemble performs a random walk in potential energy space and can overcome this difficulty. From only one simulation run, one can obtain canonical-ensemble averages of physical quantities as functions of temperature by the single-histogram and/or multiple-histogram

reweighting techniques. In this article we review uses of the generalized-ensemble algorithms in biomolecular systems. Three well-known methods, namely, multicanonical algorithm, simulated tempering, and replica-exchange method, are described first. Both Monte Carlo and molecular dynamics versions of the algorithms are given. We then present three new generalized-ensemble algorithms that combine the merits of the above methods. The effectiveness of the methods for molecular simulations in the protein **folding problem** is tested with short peptide systems.
Copyright 2001 John Wiley & Sons, Inc. Biopolymers (Pept Sci) 60: 96-123, 2001

L3 ANSWER 5 OF 36 MEDLINE
AN 2000478903 MEDLINE
DN 20484166 PubMed ID: 11027486
TI Is the unfolded state the Rosetta Stone of the protein **folding problem**?.
AU Hammarstrom P; Carlsson U
CS IFM-Department of Chemistry, Linkoping University, Linkoping, S-581 83, Sweden.
SO BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, (2000 Sep 24) 276 (2) 393-8. Ref: 40
Journal code: 0372516. ISSN: 0006-291X.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LA English
FS Priority Journals
EM 200010
ED Entered STN: 20010322
Last Updated on STN: 20010322
Entered Medline: 20001027
AB Solving the protein **folding problem** is one of the most challenging tasks in the post genomic era. Identification of folding-initiation sites is very important in order to understand the protein folding mechanism. Detection of residual structure in unfolded proteins can yield important clues to the initiation sites in protein folding. A substantial number of studied proteins possess residual structure in hydrophobic regions clustered together in the protein core. These stable structures can work as seeds in the folding process. In addition, local preferences for secondary structure in the form of turns for beta-sheet initiation and helical turns for alpha-helix formation can guide the folding reaction. In this respect the unfolded states, studied at increasing structural resolution, can be the Rosetta Stone of the protein **folding problem**.
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L3 ANSWER 6 OF 36 MEDLINE
AN 2001041022 MEDLINE
DN 20400935 PubMed ID: 10940248
TI Protein folding intermediates and pathways studied by hydrogen exchange.
AU Englander S W
CS Johnson Research Foundation, Philadelphia, Pennsylvania, USA.. walter@HX2.Med.upenn.Edu
SO ANNUAL REVIEW OF BIOPHYSICS AND BIOMOLECULAR STRUCTURE, (2000) 29 213-38. Ref: 146
Journal code: 9211097. ISSN: 1056-8700.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, ACADEMIC)
LA English
FS Priority Journals
EM 200012

ED Entered STN: 20010322
Last Updated on STN: 20010322
Entered Medline: 20001207

AB In order to solve the immensely difficult protein-**folding problem**, it will be necessary to characterize the barriers that slow folding and the intermediate structures that promote it. Although protein-folding intermediates are not accessible to the usual structural studies, hydrogen exchange (HX) methods have been able to detect and characterize intermediates in both kinetic and equilibrium modes--as transient kinetic folding intermediates on a subsecond time scale, as labile equilibrium molten globule intermediates under destabilizing conditions, and as infinitesimally populated intermediates in the high free-energy folding landscape under native conditions. Available results consistently indicate that protein-folding landscapes are dominated by a small number of discrete, metastable, native-like partially unfolded forms (PUFs). The PUFs appear to be produced, one from another, by the unfolding and refolding of the protein's intrinsically cooperative secondary structural elements, which can spontaneously create stepwise unfolding and refolding pathways. Kinetic experiments identify three kinds of barrier processes: (a) an initial intrinsic search-nucleation-collapse process that prepares the chain for intermediate formation by pinning it into a condensed coarsely native-like topology; (b) smaller search-dependent barriers that put the secondary structural units into place; and (c) optional error-dependent misfold-reorganization barriers that can cause slow folding, intermediate accumulation, and folding heterogeneity. These conclusions provide a coherent explanation for the grossly disparate folding behavior of different globular proteins in terms of distinct folding pathways.

L3 ANSWER 7 OF 36 MEDLINE
AN 1999290833 MEDLINE
DN 99290833 PubMed ID: 10361090
TI Exposing the kinetic traps in RNA folding.
AU Treiber D K; Williamson J R
CS Department of Molecular Biology, Skaggs Institute for Chemical Biology, The Scripps Research Institute, La Jolla, CA 92037, USA.. treiber@scripps.edu
SO CURRENT OPINION IN STRUCTURAL BIOLOGY, (1999 Jun) 9 (3) 339-45. Ref: 47
Journal code: 9107784. ISSN: 0959-440X.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LA English
FS Priority Journals
EM 199907
ED Entered STN: 19990727
Last Updated on STN: 19990727
Entered Medline: 19990712

AB Large ribozymes fold on a 'glacial' timescale compared to the folding of their protein counterparts. The sluggish folding exhibited by large RNAs results from the formation of kinetically trapped, misfolded intermediates, which are nonessential features of the folding mechanism. Newly developed mutant ribozymes that avoid kinetic traps should facilitate the study of the RNA **folding problem**.

L3 ANSWER 8 OF 36 MEDLINE
AN 1999337584 MEDLINE
DN 99337584 PubMed ID: 10407402
TI Beyond proteins.
AU Robson B
CS Computational Biology Center, IBM T. J. Watson Research Center, 30 Saw Mill River Road, Hawthorne, NY 10523, USA.. robsonb@us.ibm.com
SO TRENDS IN BIOTECHNOLOGY, (1999 Aug) 17 (8) 311-5. Ref: 22
Journal code: 8310903. ISSN: 0167-7799.

CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LA English
FS Priority Journals
EM 199909
ED Entered STN: 19991012
Last Updated on STN: 19991012
Entered Medline: 19990928
AB Increased understanding of the biological principles of protein structure and folding, combined with advances in protein-synthetic chemistry, should not only allow us to borrow from biology but also to depart from it and so produce protein-like, but non-protein, molecules and molecular devices. However, radical departures from protein-like forms into more-robust and truly novel 'smart' polymers and materials first require a solution to the protein-**folding problem** using only fundamental physicochemical principles. Any such practical solution may not come from raw computing power alone but rather from a deeper understanding of topological principles.

L3 ANSWER 9 OF 36 MEDLINE
AN 2000020729 MEDLINE
DN 20020729 PubMed ID: 10550208
TI How RNA folds.
AU Tinoco I Jr; Bustamante C
CS Department of Chemistry, University of California Berkeley, Berkeley, CA 94720-1460, USA.
NC GM 10840 (NIGMS)
GM 32543 (NIGMS)
SO JOURNAL OF MOLECULAR BIOLOGY, (1999 Oct 22) 293 (2) 271-81. Ref: 55
Journal code: 2985088R. ISSN: 0022-2836.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LA English
FS Priority Journals
EM 199911
ED Entered STN: 20000111
Last Updated on STN: 20000111
Entered Medline: 19991119
AB We describe the RNA **folding problem** and contrast it with the much more difficult protein **folding problem**. RNA has four similar monomer units, whereas proteins have 20 very different residues. The folding of RNA is hierarchical in that secondary structure is much more stable than tertiary folding. In RNA the two levels of folding (secondary and tertiary) can be experimentally separated by the presence or absence of Mg2+. Secondary structure can be predicted successfully from experimental thermodynamic data on secondary structure elements: helices, loops, and bulges. Tertiary interactions can then be added without much distortion of the secondary structure. These observations suggest a folding algorithm to predict the structure of an RNA from its sequence. However, to solve the RNA **folding problem** one needs thermodynamic data on tertiary structure interactions, and identification and characterization of metal-ion binding sites. These data, together with force versus extension measurements on single RNA molecules, should provide the information necessary to test and refine the proposed algorithm.

L3 ANSWER 10 OF 36 MEDLINE
AN 1999257331 MEDLINE
DN 99257331 PubMed ID: 10322208
TI New Monte Carlo algorithms for protein folding.

AU Hansmann U H; Okamoto Y
CS Department of Physics Michigan Technological University, Houghton, MI 49931-1295, USA.. hansmann@mtu.edu
SO CURRENT OPINION IN STRUCTURAL BIOLOGY, (1999 Apr) 9 (2) 177-83. Ref: 84
Journal code: 9107784. ISSN: 0959-440X.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LA English
FS Priority Journals
EM 199908
ED Entered STN: 19990910
Last Updated on STN: 19990910
Entered Medline: 19990820
AB Over the past three decades, a number of powerful simulation algorithms have been introduced to the protein **folding problem**.
For many years, the emphasis has been placed on how to both overcome the multiple minima problem and find the conformation with the global minimum potential energy. Since the new view of the protein folding mechanism (based on the free energy landscape of the protein system) arose in the past few years, however, it is now of interest to obtain a global knowledge of the phase space, including the intermediate and denatured states of proteins. Monte Carlo methods have proved especially valuable for these purposes. As well as new, powerful optimization techniques, novel algorithms that can sample much a wider phase space than conventional methods have been established.

=> d 11-20 bib ab

L3 ANSWER 11 OF 36 MEDLINE
AN 1998195429 MEDLINE
DN 98195429 PubMed ID: 9526123
TI Denatured states of yeast phosphoglycerate kinase.
AU Damaschun G; Damaschun H; Gast K; Zirwer D
CS Institut fur Biologie der Humboldt-Universitat zu Berlin, Germany.. gdamasc@mdc-berlin.de
SO BIOCHEMISTRY, (1998 Mar) 63 (3) 259-75. Ref: 98
Journal code: 0376536. ISSN: 0006-2979.
CY RUSSIA: Russian Federation
DT Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LA English
FS Priority Journals
EM 199808
ED Entered STN: 19980820
Last Updated on STN: 19980820
Entered Medline: 19980811
AB Structures of proteins in unfolded states have important implications for the protein **folding problem** and for the translocation of polypeptide chains. Acid-denatured, cold-denatured, and 6 M guanidine hydrochloride (GuHCl) denatured yeast phosphoglycerate kinase (PGK) are ensembles of flexible unfolded molecules with rapidly interconverting structures of the individual polypeptide chains. They differ, however, in their physical properties, such as in coil size and in stiffness over a short distance along the chain. These properties of polypeptide chains can be described well by persistence statistics. A solution containing 0.7 M GuHCl at 4.5 degrees C is nearly a Theta-solvent for PGK. By contrast, 6 M GuHCl is a good solvent for PGK. Acid-denatured PGK at low ionic strength has the most expanded and stiffest chains. The conformation of heat-denatured PGK should be more compact than that of random walk chains at the Theta-point, as can be inferred from measurements on other proteins. Investigations of heat-denatured PGK by scattering methods are

unfeasible due to aggregation of the protein. The persistence length as a measure of chain stiffness varies between a = 1.74 nm for cold-denatured PGK and a = 3.0 nm for acid-denatured PGK. The distribution functions of the gyration radii were calculated from the X-ray scattering data for all unfolded states and compared with the radius of gyration of the natively folded molecule.

L3 ANSWER 12 OF 36 MEDLINE
AN 1999106815 MEDLINE
DN 99106815 PubMed ID: 9890141
TI Protein structure prediction and design.
AU Morea V; Leplae R; Tramontano A
CS IRBM P. Angeletti, Pomezia, Rome, Italy.
SO BIOTECHNOLOGY ANNUAL REVIEW, (1998) 4 177-214. Ref: 160
Journal code: 9616443.
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, ACADEMIC)
LA English
FS Priority Journals
EM 199902
ED Entered STN: 19990216
Last Updated on STN: 19990216
Entered Medline: 19990202
AB Proteins have a unique native conformation, which can be proven in many instances to be determined by the amino acid sequence alone. The **folding problem**, that is the understanding of how the amino acid sequence directs folding, is still unsolved, despite more than 30 years of effort. However, many new methods have appeared in the past few years. This chapter describes the different principles underlying them and tries to give an overview of their successes and pitfalls.

L3 ANSWER 13 OF 36 MEDLINE
AN 1998179825 MEDLINE
DN 98179825 PubMed ID: 9519299
TI Simplified proteins: minimalist solutions to the 'protein **folding problem**'.
AU Plaxco K W; Riddle D S; Grantcharova V; Baker D
CS Department of Biochemistry, University of Washington, Seattle 98195, USA.. kwp@elina.bchem.washington.edu
SO CURRENT OPINION IN STRUCTURAL BIOLOGY, (1998 Feb) 8 (1) 80-5. Ref: 48
Journal code: 9107784. ISSN: 0959-440X.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LA English
FS Priority Journals
EM 199805
ED Entered STN: 19980514
Last Updated on STN: 19980514
Entered Medline: 19980501
AB Recent research has suggested that stable, native proteins may be encoded by simple sequences of fewer than the full set of 20 proteogenic amino acids. Studies of the ability of simple amino acid sequences to encode stable, topologically complex, native conformations and to fold to these conformations in a biologically relevant time frame have provided insights into the sequence determinants of protein structure and folding kinetics. They may also have important implications for protein design and for theories of the origins of protein synthesis itself.

L3 ANSWER 14 OF 36 MEDLINE
AN 1998179824 MEDLINE
DN 98179824 PubMed ID: 9519298

TI Pathways for protein folding: is a new view needed?.
AU Pande V S; Grosberg AYu; Tanaka T; Rokhsar D S
CS Department of Physics, University of California at Berkeley, CA 94720-7300, USA.. vijay@physics.berkeley.edu
SO CURRENT OPINION IN STRUCTURAL BIOLOGY, (1998 Feb) 8 (1) 68-79. Ref: 114
Journal code: 9107784. ISSN: 0959-440X.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LA English
FS Priority Journals
EM 199805
ED Entered STN: 19980514
Last Updated on STN: 19980514
Entered Medline: 19980501
AB Theoretical studies using simplified models of proteins have shed light on the general heteropolymeric aspects of the **folding problem**. Recent work has emphasized the statistical aspects of folding pathways. In particular, progress has been made in characterizing the ensemble of transition state conformations and elucidating the role of intermediates. These advances suggest a reconciliation between the new ensemble approaches and the classical view of a folding pathway.

L3 ANSWER 15 OF 36 MEDLINE
AN 1998357356 MEDLINE
DN 98357356 PubMed ID: 9692327
TI Protein design: on the threshold of functional properties.
AU Tuchscherer G; Scheibler L; Dumy P; Mutter M
CS Institute of Organic Chemistry, University of Lausanne, Switzerland.
SO BIOPOLYMERS, (1998) 47 (1) 63-73. Ref: 58
Journal code: 0372525. ISSN: 0006-3525.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LA English
FS Priority Journals
EM 199809
ED Entered STN: 19980917
Last Updated on STN: 19990129
Entered Medline: 19980908
AB The ultimate goal in protein de novo design is the creation of novel macromolecules with tailor-made receptor, sensory, and catalytic functions. Despite considerable progress in understanding basic rules of secondary structure formation and protein stability, the well-known protein **folding problem** is still far from being solved and, in general, only a limited number of designed proteins are folded uniquely. In this article the state-of-the-art in protein design is demonstrated on some selected examples, indicating that the construction of protein-like macromolecules mimicking some essential features of natural proteins seems to be within reach. Thus, protein design and mimicry has become an interdisciplinary challenge with most intriguing perspectives.

L3 ANSWER 16 OF 36 MEDLINE
AN 97348223 MEDLINE
DN 97348223 PubMed ID: 9204274
TI Protein-facilitated RNA folding.
AU Weeks K M
CS Department of Chemistry, University of North Carolina, Chapel Hill 27599-3290, USA.. weeks@unc.edu
SO CURRENT OPINION IN STRUCTURAL BIOLOGY, (1997 Jun) 7 (3) 336-42. Ref: 58
Journal code: 9107784. ISSN: 0959-440X.
CY ENGLAND: United Kingdom

DT Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LA English
FS Priority Journals
EM 199708
ED Entered STN: 19970825
Last Updated on STN: 19970825
Entered Medline: 19970808
AB In the absence of protein collaborators, both simple and complex RNAs often misfold or are unfolded. Biologically important RNAs solve their **folding problem**, in part, using the assistance of chaperone and cofactor proteins. Recent work emphasizes several rules for RNA-protein complexes: formation involves induced fit; many large RNAs fold slowly; and ribonucleoprotein assembly requires multiple steps. Finally, protein binding can introduce thermodynamic side effects.

L3 ANSWER 17 OF 36 MEDLINE
AN 97398939 MEDLINE
DN 97398939 PubMed ID: 9255068
TI RNA seeing double: close-packing of helices in RNA tertiary structure.
AU Strobel S A; Doudna J A
CS Department of Molecular Biophysics and Biochemistry, Yale University, New Haven, CT 06520, USA.
NC GM22778-21 (NIGMS)
GM54839-01 (NIGMS)
SO TRENDS IN BIOCHEMICAL SCIENCES, (1997 Jul) 22 (7) 262-6. Ref: 49
Journal code: 7610674. ISSN: 0968-0004.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LA English
FS Priority Journals
EM 199709
ED Entered STN: 19970922
Last Updated on STN: 20000303
Entered Medline: 19970905
AB Structured RNA molecules play essential roles in RNA processing, chromosome maintenance and protein biosynthesis. RNA necessarily uses different strategies than proteins for folding and assembly of complex architectures. The RNA-**folding problem** is largely an issue of helical packing: how does RNA organize and pack short, double-helical segments to produce active sites and recognition motifs for proteins? Noncanonical base pairs, metal ions and 2'-hydroxyl groups are key elements in RNA higher-order structure formation.

L3 ANSWER 18 OF 36 MEDLINE
AN 97414929 MEDLINE
DN 97414929 PubMed ID: 9269572
TI The Levinthal paradox: yesterday and today.
AU Karplus M
CS Laboratoire de Chimie Biophysique, Institute le Bel, Universite Louis Pasteur, Strasbourg, France.. marci@brel.u-strasbg.fr
SO FOLDING AND DESIGN, (1997) 2 (4) S69-75. Ref: 75
Journal code: 9604387. ISSN: 1359-0278.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LA English
FS Priority Journals
EM 199710
ED Entered STN: 19971013
Last Updated on STN: 19971013

Entered Medline: 19971001

AB A change in the perception of the protein **folding problem** has taken place recently. The nature of the change is outlined and the reasons for it are presented. An essential element is the recognition that a bias toward the native state over much of the effective energy surface may govern the folding process. This has replaced the random search paradigm of Levinthal and suggests that there are many ways of reaching the native state in a reasonable time so that a specific pathway does not have to be postulated. The change in perception is due primarily to the application of statistical mechanical models and lattice simulations to protein folding. Examples of lattice model results on protein folding are presented. It is pointed out that the new optimism about the protein **folding problem** must be complemented by more detailed studies to determine the structural and energetic factors that introduce the biases which make possible the folding of real proteins.

L3 ANSWER 19 OF 36 MEDLINE
AN 97184701 MEDLINE
DN 97184701 PubMed ID: 9032055
TI The prion **folding problem**.
AU Harrison P M; Bamborough P; Daggett V; Prusiner S B; Cohen F E
CS University of California, Box Number 450, San Francisco, CA-94143, USA.
SO CURRENT OPINION IN STRUCTURAL BIOLOGY, (1997 Feb) 7 (1) 53-9. Ref: 51
Journal code: 9107784. ISSN: 0959-440X.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LA English
FS Priority Journals
EM 199703
ED Entered STN: 19970327
Last Updated on STN: 19970327
Entered Medline: 19970319
AB Prion diseases are neurodegenerative disorders in which dramatic conformational change in the structure of the prion protein is the fundamental event. This structural transition involves the loss of substantial alpha-helical content and the acquisition of beta-sheet structure. A convergence of recent biological and structural studies argues that the mechanism underlying the prion diseases is truly unprecedented.

L3 ANSWER 20 OF 36 MEDLINE
AN 97181651 MEDLINE
DN 97181651 PubMed ID: 9029812
TI Gramicidin channels--a solvable membrane "protein" **folding problem**.
AU Andersen O S; Saberwal G; Greathouse D V; Koeppe R E 2nd
CS Department of Physiology and Biophysics, Cornell University Medical College, New York, NY 10021, USA.
NC GM21342 (NIGMS)
GM34968 (NIGMS)
SO INDIAN JOURNAL OF BIOCHEMISTRY AND BIOPHYSICS, (1996 Oct) 33 (5) 331-42.
Ref: 79
Journal code: 0310774. ISSN: 0301-1208.
CY India
DT Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LA English
FS Priority Journals
EM 199703
ED Entered STN: 19970414
Last Updated on STN: 19970414

Entered Medline: 19970328

AB The linear gramicidins are peptide antibiotics that form cation-selective channels in lipid bilayers. Gramicidin channels have very well-defined functional characteristics, and the structure of membrane-spanning gramicidin A channels is known at atomic resolution. These features make the gramicidins well suited to study how the amino acid sequence encodes the structure and function of a membrane-spanning channel. We show how one can use electrophysiological measurements to obtain structural information about conducting channels and to quantify the conformational preferences of sequence-substituted gramicidin mutants.

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---Logging off of STN---

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